

## SEQUENCE LISTING

DT04 Rec'd PCT/PTO 14 OCT 2004

&lt;110&gt; Evotec NeuroSciences GmbH

&lt;120&gt; Diagnostic and therapeutic use of a Golgi protein for neurodegenerative diseases

&lt;130&gt; 030810wo

&lt;140&gt; PCT/EP03/03958

&lt;141&gt; 2003-04-16

&lt;160&gt; 27

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: golgin-245 cDNA fragment

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36

&lt;210&gt; 2

&lt;211&gt; 2228

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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115 120 125Gly Asn Ser Asp Ser Leu Asn Lys Glu Gln Leu Ile Gln Arg Leu Arg  
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885

890

895

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Phe Asn Thr Gln Leu Ala Gln Lys Glu Gln Glu Leu Glu Met Thr Ile 2005	2010	2015
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Thr Met Ala Lys Val Ile Thr Thr Val Leu Lys Phe Pro Asp Asp Gln 2195	2200	2205
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&lt;210&gt; 3

&lt;211&gt; 7636

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: cDNA of the  
human golgin-245 splice variant 1

&lt;400&gt; 3

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Glu Ser Leu Val Arg Thr Ser Ser Arg Glu Ser Leu Asn Arg Leu Asp
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Lys Glu Ile Thr Val Met Val Glu Lys His Lys Thr Glu Leu Glu Ser	625	630	635
Leu Lys His Gln Gln Asp Ala Leu Trp Thr Glu Lys Leu Gln Val Leu	645	650	655
Lys Gln Gln Tyr Gln Thr Glu Met Glu Lys Leu Arg Glu Lys Cys Glu	660	665	670
Gln Glu Lys Glu Thr Leu Leu Lys Asp Lys Glu Ile Ile Phe Gln Ala	675	680	685
His Ile Glu Glu Met Asn Glu Lys Thr Leu Glu Lys Leu Asp Val Lys	690	695	700
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Val Glu Asn Leu Glu Ala Asp Ile Lys Arg Ser Glu Gly Glu Leu Gln	805	810	815
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&lt;210&gt; 8

&lt;211&gt; 2252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met 1	Phe	Lys	Lys	Leu 5	Lys	Gln	Lys	Ile	Ser 10	Glu	Glu	Gln	Gln	Gln	Leu 15
Gln	Gln	Ala	Leu 20	Ala	Pro	Ala	Gln	Ala 25	Ser	Ser	Asn	Ser	Ser 30	Thr	Pro
Thr	Arg	Met 35	Arg	Ser	Arg	Thr	Ser 40	Ser	Phe	Thr	Glu	Gln 45	Leu	Asp	Glu
Gly	Thr 50	Pro	Asn	Arg	Glu	Asn 55	Ala	Ser	Thr	His	Ala 60	Ser	Lys	Ser	Pro
Asp 65	Ser	Val	Asn	Gly	Ser 70	Glu	Pro	Ser	Ile	Pro 75	Gln	Ser	Gly	Asp	Thr 80
Gln	Ser	Phe	Ala	Gln 85	Lys	Leu	Gln	Leu	Arg 90	Val	Pro	Ser	Val	Glu 95	Ser
Leu	Phe	Arg	Ser 100	Pro	Ile	Lys	Glu	Ser 105	Leu	Phe	Arg	Ser	Ser 110	Ser	Lys
Glu	Ser	Leu 115	Val	Arg	Thr	Ser	Ser 120	Arg	Glu	Ser	Leu	Asn 125	Arg	Leu	Asp
Leu	Asp 130	Ser	Ser	Thr	Ala	Ser 135	Phe	Asp	Pro	Pro	Ser 140	Asp	Met	Asp	Ser
Glu 145	Ala	Glu	Asp	Leu	Val 150	Gly	Asn	Ser	Asp	Ser 155	Leu	Asn	Lys	Glu	Gln 160
Leu	Ile	Gln	Arg	Leu 165	Arg	Arg	Met	Glu	Arg 170	Ser	Leu	Ser	Ser	Tyr 175	Arg
Gly	Lys	Tyr	Ser 180	Glu	Leu	Val	Thr	Ala 185	Tyr	Gln	Met	Leu	Gln 190	Arg	Glu
Lys	Lys	Lys 195	Leu	Gln	Gly	Ile	Leu 200	Ser	Gln	Ser	Gln	Asp 205	Lys	Ser	Leu
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Asp	Gly 290	Glu	Pro	Val	Val	Glu 295	Asp	Gly	Thr	Ser	Val 300	Lys	Thr	Leu	Glu
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Met	Lys	Glu	Glu	Glu	Ile	Ala	Gln	Leu	Arg	Ser	Arg	Ile	Lys	Gln	Met
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Thr	Thr	Gln	Gly	Glu	Glu	Leu	Arg	Glu	Gln	Lys	Glu	Lys	Ser	Glu	Arg
			420					425						430	
Ala	Ala	Phe	Glu	Glu	Leu	Glu	Lys	Ala	Leu	Ser	Thr	Ala	Gln	Lys	Thr
		435					440					445			
Glu	Glu	Ala	Arg	Arg	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	Gln	Ile	Lys
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Thr	Ile	Glu	Lys	Thr	Ser	Glu	Glu	Glu	Arg	Ile	Ser	Leu	Gln	Gln	Glu
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Leu	Ser	Arg	Val	Lys	Gln	Glu	Val	Val	Asp	Val	Met	Lys	Lys	Ser	Ser
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			500					505					510		
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		515					520					525			
Phe	Gln	Glu	Gln	Met	Lys	Val	Ala	Leu	Glu	Lys	Ser	Gln	Ser	Glu	Tyr
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Glu	Leu	Glu	Leu	Gln	Lys	Lys	Ala	Ile	Leu	Thr	Glu	Ser	Glu	Asn	Lys
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			580					585					590		
Glu	Leu	Glu	Ser	Ser	Leu	Glu	Lys	Ser	Leu	Gln	Glu	Asn	Lys	Asn	Gln
		595					600					605			
Ser	Lys	Asp	Leu	Ala	Val	His	Leu	Glu	Ala	Glu	Lys	Asn	Lys	His	Asn
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Lys	Glu	Ile	Thr	Val	Met	Val	Glu	Lys	His	Lys	Thr	Glu	Leu	Glu	Ser
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Leu	Lys	His	Gln	Gln	Asp	Ala	Leu	Trp	Thr	Glu	Lys	Leu	Gln	Val	Leu
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Lys	Gln	Gln	Tyr	Gln	Thr	Glu	Met	Glu	Lys	Leu	Arg	Glu	Lys	Cys	Glu
			660					665					670		
Gln	Glu	Lys	Glu	Thr	Leu	Leu	Lys	Asp	Lys	Glu	Ile	Ile	Phe	Gln	Ala
		675					680					685			
His	Ile	Glu	Glu	Met	Asn	Glu	Lys	Thr	Leu	Glu	Lys	Leu	Asp	Val	Lys
	690					695					700				
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Ala Arg His Lys Leu Glu Glu Glu Leu Ser Val Leu Lys Asp Gln Thr  
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 Ile Gln Arg Thr Glu Lys Ala Leu Lys Asp Gln Ile Asn Gln Leu Glu  
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 Leu Leu Leu Lys Glu Arg Asp Lys His Leu Lys Glu His Gln Ala His  
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 Val Glu Asn Leu Glu Ala Asp Ile Lys Arg Ser Glu Gly Glu Leu Gln  
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 Gln Ala Ser Ala Lys Leu Asp Val Phe Gln Ser Tyr Gln Ser Ala Thr  
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 Lys Leu Leu Asp Leu Glu Thr Glu Arg Ile Leu Leu Thr Lys Gln Val  
 850 855 860  
 Ala Glu Val Glu Ala Gln Lys Lys Asp Val Cys Thr Glu Leu Asp Ala  
 865 870 875 880  
 His Lys Ile Gln Val Gln Asp Leu Met Gln Gln Leu Glu Lys Gln Asn  
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 Ser Glu Met Glu Gln Lys Val Lys Ser Leu Thr Gln Val Tyr Glu Ser  
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 Lys Leu Glu Asp Gly Asn Lys Glu Gln Glu Gln Thr Lys Gln Ile Leu  
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 His Ile Leu Asn Glu Glu Tyr Glu Thr Lys Phe Lys Asn Gln Glu Lys  
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Ser Arg Phe Thr Gln His Gln Asn Thr Val Lys Glu Leu Gln Ile Gln	1475	1480	1485
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Asn Leu Glu Thr Glu Leu Lys Ser Gln Thr Ala Arg Ile Met Glu Leu	1540	1545	1550
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<223> Description of Artificial Sequence: primer for the  
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<223> Description of Artificial Sequence: primer for the  
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